

## **TITLE OF THE INVENTION**

### **SMALL AND CYSTEINE RICH ANTIFUNGAL DEFENSIN AND THIONIN- LIKE PROTEIN GENES HIGHLY EXPRESSED IN THE INCOMPATIBLE INTERACTION**

This is a division of application Serial Number 09/442,631 filed 18 November 1999.

## **BACKGROUND OF THE INVENTION**

The present invention related to two cDNA clones, designated to *PepDef* (pepper defensin protein gene) and *PepThi* (pepper thionin-like protein gene) and individual component; thereof including its coding region and its gene product; modification thereto; application of said gene, coding region and modification thereto; DNA construct, vectors and transformed plants each comprising the gene or part thereof.

Plants have developed defense mechanisms to defend themselves against phytopathogens. Plants' first responses to pathogen infection include fortification of cell walls for physical barriers by deposition of lignin (Dean and Kuc, 1988) and by oxidative cross-linking (Brisson *et al.*, 1994) as well as the hypersensitive reaction (HR). HR causes a rapid cell death of infected tissues to halt further colonization by pathogens (Goodman and Novacky, 1994). The next array of defense strategies includes the production of antimicrobial phytoalexins (van Etten *et al.*, 1989), pathogenesis-related (PR) proteins (Linthorst, 1991; Ponstein *et al.*, 1994), and cysteine (Cys)-rich proteins, such as lipid transfer protein (Garcia-Olmedo *et al.*, 1995) and thionins (Bohlmann,

1994).

Thionins are small, highly basic, Cys-rich proteins that show antimicrobial activity and seem to have a role in plant defense against fungi and bacteria. The overexpression of the THI2.1 thionin in *Arabidopsis* enhanced resistance to a phytopathogenic fungus (Epple *et al.*, 1997). The overexpression of  $\alpha$ -hordothionin in tobacco also enhanced resistance to a phytopathogenic bacterium (Carmona *et al.*, 1993). In addition, during barley and powdery mildew interactions, the accumulation of thionins was higher in the incompatible interaction than in the compatible one (Ebrahim-Nesbat *et al.*, 1993).

The thionins contain a signal sequence, the thionin domain and an acid polypeptide domain as well as the conserved Cys residues (Bohlmann *et al.*, 1994). A new class of Cys-rich antimicrobial protein,  $\gamma$ -thionin, has a similar size (5 kD) and the same number of disulfide bridges as thionins. However, since  $\gamma$ -thionins do not have significant sequence homologies with thionins, they have been described as plant defensins (Terras *et al.*, 1995). Both defensin and thionin genes in *Arabidopsis* are inducible via a salicylic acid-independent pathway different from that for PR proteins (Epple *et al.*, 1995; Penninckx *et al.*, 1996).

Fruit ripening represents a genetically synchronized process that involves developmental events unique to plant species. Generally, ripe fruits are susceptible to pathogen attack (Swinburne, 1983; Prusky *et al.*, 1991). Therefore, fruit as one of the reproductive organs of the plants must be protected from pathogens to maintain their

integrity and seed maturation. Several antifungal proteins that are responsible for protection against pathogens during fruit ripening have been identified (Fils-Lycaon *et al.*, 1996; Meyer *et al.*, 1996; Salzman *et al.*, 1998). Also, PR proteins are developmentally expressed during the formation of flowers (Lotan *et al.*, 1989; Côté *et al.*, 1991).

*Colletotrichum gloeosporioides* (Penz.) causes anthracnose diseases in many plant species (Daykin, 1984; Dodds *et al.*, 1991; Prusky *et al.*, 1991). *C. gloeosporioides* is the most prevalent species among *C. acutatum*, *C. coccodes*, *C. dematium*, *C. gloeosporioides*, and *G. cingulata* to cause anthracnose diseases on pepper (*Capsicum annuum* L.) (Kim *et al.*, 1986; Manandhar *et al.*, 1995). In previous study, we found that the unripe-mature-green fruit of pepper cv. Nokkwang interacted compatibly with *C. gloeosporioides*, whereas the interaction of the ripe-red fruits with fungus was incompatible (Oh *et al.*, 1998). To investigate the activation of defense-related genes from the incompatible-pepper fruit upon *C. gloeosporioides* infection, we isolated a defensin gene and a thionin-like gene by using mRNA differential display. The regulation of these Cys-rich protein genes was studied during fruit ripening and in the initial infection process during the compatible and incompatible interactions. We report here what appears to be the first case of a defensin gene and a thionin-like gene induced via different signal transduction pathways in a plant and fungus interaction.

## SUMMARY OF THE INVENTION

The present invention relates to two cDNA clones, designated to a defensin gene, *PepDef*, and a thionin-like gene, *PepThi*, the sequences of which are depicted in SEQ ID No. 1 and No. 3, respectively. The anthracnose fungus, *C. gloeosporioides*, interacts incompatibly with ripe fruits of pepper (*Capsicum annuum*). It interacts compatibly with the unripe-mature fruits. We isolated *PepDef* and *PepThi* expressed in the incompatible interaction by using mRNA differential display method. Both genes were developmentally regulated during fruit ripening, organ-specifically regulated, and differentially induced during the compatible and incompatible interactions. The expression of *PepThi* gene was rapidly induced in the incompatible-ripe fruit upon fungal infection. The fungal-inducible *PepThi* gene is highly inducible only in the unripe fruit by salicylic acid. In both ripe and unripe fruits, it was induced by wounding, but not by jasmonic acid. The expression of *PepDef* gene is enhanced in the unripe fruit by jasmonic acid, while suppressed in the ripe fruit. These results suggest that both small and cysteine-rich protein genes are induced via different signal transduction pathways during fruit ripening to protect the reproductive organs against biotic and abiotic stresses. The *PepDef* and *PepThi* can be cloned into an expression vector to produce a recombinant DNA expression system suitable for insertion into cells to form a transgenic plant transformed with these genes. In addition, the *PepDef* and *PepThi* genes of this invention can be also used to produce transgenic plants that exhibit enhanced resistance against phytopathogens, including fungi, bacteria, viruses, nematode, mycoplasma-like organisms, parasitic higher plants, flagellate protozoa, and insects.

## BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1. Alignment of the deduced amino acid sequences from *PepDef* (GenBank accession number X95363) and *PepThi* cDNAs (AF112443) of pepper (Meyer *et al.*, 1996) with other thionins from tomato (*Lycopersicon esculentum*, U20591; Milligan and Gasser, 1995), *Nicotiana excelsior* (AB005266), tobacco (*N. tabacum*, Z11748; Gu *et al.*, 1992), and *N. paniculata* (AB005250). The conserved cysteine arrangement - C(...)C-X-X-X-C(...)G-X-C(...)C-X-C- is indicated by arrows.

FIG. 2. Expression and induction of *PepDef* and *PepThi* genes from various organs of pepper by *Colletotrichum gloeosporioides* infections and wounding. RNAs were isolated from ripe fruit (R), unripe fruit (U), leaf, stem, and root at 24 h after the treatments of fungal infection (FI) and wounding (W). In addition, RNAs of both ripe and unripe fruits at 48 h after wounding (R48 and U48) were isolated. Ten  $\mu\text{l}$  at  $5 \times 10^5$  conidia/ml of *C. gloeosporioides* was used for the inoculation of various pepper organs. Organs treated with 10  $\mu\text{l}$  sterile-water except fungal spores for 24 h were used as the controls (C).

FIG. 3. Differential induction of *PepDef* and *PepThi* genes from both ripe and unripe fruits of pepper by *Colletotrichum gloeosporioides* infections. RNAs were isolated from both ripe (incompatible interaction) and unripe fruits (compatible interaction) after the fungal infection with time course. Time is indicated in h after infection.

FIG. 4. Induction and suppression of *PepDef* and *PepThi* genes from both ripe and

unripe fruits of pepper by exogenous salicylic acid (SA) and jasmonic acid (JA) treatments. RNAs were isolated from both ripe (R) and unripe fruits (U) treated with SA (1 = 0.5 mM, 2 = 5mM) and JA (3 = 4  $\mu$ M, 4 = 40  $\mu$ M) for 24 h. Fruits treated with 10  $\mu$ l sterile-water except fungal spores for 24 h were used as the control (C).

### DETAILED DESCRIPTION OF THE INVENTION

The present invention has identified two cDNA clones, designated to *PepDef* and *PepThi*, from the incompatible interaction between pepper and the pepper anthracnose fungus *Colletotrichum gloeosporioides* using mRNA differential display and cDNA library screening.

The *PepThi* cDNA is 506 bp in length with 9 bp of 5'-untranslated region and 245 bp of 3'-untranslated region including the poly(A) tail (GenBank AF112443). The *PepThi* clone represented a full-length cDNA of the 0.5 kb transcript identified by RNA gel blot analysis. The cDNA contained one open reading frame encoding a polypeptide of 9.5 kDa with 84 amino acids. The deduced amino acid sequence of *PepThi*(SEQ ID No. 4) contained an N-terminal secretory signal peptide that was cleaved after glycine at position 25 (Figure 1). *PepThi* is a Cys-rich polypeptide containing the consensus Cys arrangement -C(...)C-X-X-X-C(...)G-X-C(...)C-X-C-.

The *PepDef* cDNA is 225 bp except 5'-untranslated region and 3'-untranslated region including the poly(A) tail (X95363). The *PepDef* clone represented a full-length

cDNA of the 0.45 kb transcript identified by RNA gel blot analysis. The cDNA contained one open reading frame encoding a polypeptide of 8.5 kDa with 75 amino acids. The deduced amino acid sequence of PepDef (SEQ ID No. 3) contained an N-terminal secretory signal peptide that was cleaved after alanine at position 27 (Figure 1). PepDef is also a Cys-rich polypeptide containing the consensus Cys arrangement - C(...)C-X-X-X-C(...)G-X-C(...)C-X-C-.

The expression of *PepThi* gene was observed in ripe fruits, leaves, stems, and roots of pepper, respectively. The basal and non-induced level of *PepThi* gene was higher in the leaves and roots than in the fruits and stems. In the fruits, the *PepThi* mRNA was highly induced by fungal infection and wounding. Also, the accumulation of the *PepThi* mRNA increased in the stems with fungal infection and wounding. However, the level of *PepThi* mRNA was not significantly changed in the leaves and roots by the treatments.

The *PepDef* mRNA was not detected in leaves, stems, and roots even after fungal infection and wounding. However, the basal level of *PepDef* gene was very high in the ripe fruit, and undetectably low in the unripe fruit. Interestingly, the level of *PepDef* mRNA was reduced in the ripe fruit by fungal infection and wounding. This phenomenon was also observed in the ripe fruit by JA treatment. The accumulation of *PepDef* mRNA was not significantly induced in the unripe fruit by fungal infection and wounding for 24 h or 48 h. These results suggest that *PepDef* and *PepThi* genes are developmentally and organ-specifically regulated, and the induction by fungal infection and wounding is also subject to developmental regulation.

To examine the time course of the induction of *PepDef* or *PepThi* mRNAs in response to the fungal infection, RNA gel blot analysis was performed with the ripe and unripe fruits at 0, 3, 6, 12, 24, 48, and 72 h after inoculation (HAI) using *PepDef* and *PepThi* cDNAs as probes. The uninoculated incompatible-ripe fruit contained a basal level of *PepThi* mRNA. However, the expression of *PepThi* was rapidly induced in the ripe fruit upon fungal infection and reached a maximum at 48 and 72 HAIs. In compatible-unripe fruits, the accumulation of *PepThi* mRNA was late, at 12 HAI, and reached its maximum level at 72 HAI.

Accumulation of *PepDef* mRNA in the unripe fruit was very low. *PepDef* expression was suppressed by fungal infection in the ripe fruit. The transcript levels dropped until 48 HAI, and had begun to increase again 72 HAI. Since *PepDef* gene was highly expressed in the ripe fruit and *PepThi* gene was induced in the ripe fruit by the fungal infection, these genes may be involved in the defense mechanism during fruit ripening against the phytopathogen.

To identify inducers of *PepDef* and *PepThi* gene expression from fruits, RNA gel blot analysis was performed with unripe and ripe fruits treated with exogenous jasmonic acid (JA) and salicylic acid (SA) for 24 h. The *PepThi* mRNA was highly accumulated in the unripe fruit compared to in the ripe fruit by SA at 5 mM (Figure 4). However, JA could not significantly induce the *PepThi* mRNA in both ripe and unripe fruits. The expression level of *PepDef* mRNA was not changed in both ripe and unripe fruits by SA. Interestingly, the expression of *PepDef* mRNA by JA increased in the



unripe fruit, but decreased slightly in the ripe fruit. Taken together, these results suggest that the *PepThi* and *PepDef* genes are expressed via different signal transduction pathways during ripening.

The *PepDef* and *PepThi* genes can be cloned into an expression vector to produce a recombinant DNA expression system suitable for insertion into cells to form a transgenic plant transformed with these genes. In addition, the *PepDef* and *PepThi* genes of this invention can be also used to produce transgenic plants that exhibit enhanced resistance against phytopathogens, including fungi, bacteria, viruses, nematode, mycoplasmalike organisms, parasitic higher plants, flagellate protozoa, and insects.

## EXAMPLES

### **Fungal inoculum and plant material**

Monoconidial isolate KG13 of *C. gloeosporioides* was cultured on potato dextrose agar (Difco, USA) for 5 days in darkness at 27°C. Sterile distilled water was added and conidia were harvested through four layers of cheesecloth to remove mycelial debris. Ten µl at  $5 \times 10^5$  conidia/ml of *C. gloeosporioides* was used for the inoculation of both unripe and ripe pepper fruit as described (Oh *et al.*, 1998).

Both ripe-red and unripe-mature-green fruits of pepper cv. Nokkwang were grown and harvested under green-house conditions. For wound treatments, five healthy

ripe and unripe fruits were deeply scratched by a knife and incubated under relative humidity of 100% at 27°C in the dark. Ten µl of SA (0.5 and 5 mM) and JA (4 and 40 µM) was applied to both ripe and unripe sets of five fruits. After incubation under the condition described above, the fruits were excised to 1cm<sup>2</sup> at the application site and frozen in liquid nitrogen. Leaf, root, and stem samples were harvested from 3-week-old plants and handled as described above for fungal inoculation and wounding.

### **mRNA differential display**

Total RNA was extracted from healthy and infected ripe and unripe fruits using RNeasy Plant kit (Qiagen, Germany) according to the manufacturer's instruction. We used total RNA as template for the reverse transcriptase reaction and performed differential display with [ $\alpha^{33}\text{P}$ ]dATP instead of [ $\alpha^{35}\text{S}$ ]dATP (Liang and Pardee, 1992). Anchored primers and random-arbitrary primers were purchased from Operon Technologies (Alameda, CA, USA). PCR-amplified cDNA fragments were separated on denaturing 5% polyacrylamide gels in Tris-borate buffer. cDNAs were recovered from the gel, amplified by PCR, and cloned into pGEM-T easy vector (Promega, USA) as described (Oh *et al.*, 1995).

### **Construction and screening of cDNA library**

Poly(A)<sup>+</sup> mRNA was purified from total RNA of unripe fruits at 24 and 48 h after inoculation with *C. gloeosporioides* using Oligotex mRNA Kit (Qiagen, Germany). The cDNA library ( $2.5 \times 10^5$  plaque-forming unit with the mean insert size

of 1.2 kb) was constructed in the cloning vector  $\lambda$ ZAPII (Stratagene, Germany) according to the manufacturer's instruction.

A partial cDNA, designated pddThi, from the differential display was used as a probe to screen the *C. gloeosporioides*-induced pepper cDNA library. After three rounds of plaque hybridization, positive plaques were purified. The pBluescript SK phagemid containing cDNAs was excised *in vivo* from the ZAP Express vector using the ExAssit helper phage.

#### **DNA sequencing and homology search**

The cDNA sequencing was performed with an ALFexpress automated DNA sequencer (Pharmacia, Sweden). Analysis of nucleotide and amino acid sequences was performed using the DNASIS sequence analysis software for Windows, version 2.1 (Hitachi, Japan). The multiple sequence alignment was produced with the Clustal W program. For a homology search, cDNA sequence was compared to the NCBI non-redundant databases using the BLAST electronic mail server (Altschul *et al.*, 1997).

#### **RNA blot and hybridization**

Total RNA (10  $\mu$ g/lane) from each plant tissue used in this study was separated on 1.2% denaturing agarose gels in the presence of formaldehyde. RNA gel-blotting, hybridization and washing were conducted as described by the manufacturer of the positively charged nylon membrane employed (Hybond N<sup>+</sup>; Amersham, UK).

Radiolabeled probes were prepared with [ $\alpha^{32}\text{P}$ ]dCTP (Amersham) using a random primer-labeling kit (Boehringer Mannheim, Germany).

### **Cloning and characterization of thionin-like cDNAs**

*C. gloeosporioides* showed the incompatible interaction with ripe-red fruits of pepper and the compatible interaction with unripe-mature-green fruits (Oh et al., 1998). We isolated several cDNAs induced from the ripe fruit, but not from the unripe fruit by the fungal infection using mRNA differential display. By nucleotide sequence analysis of cDNAs, two cDNA fragments were identified to be thionin homologs. One cDNA was full length and was similar to *j1-1* cDNA that encodes a fruit specific defensin (Meyer et al., 1996). We named the defensin as *PepDef* (pepper defensin). Another cDNA fragment, designated pddThi, showed homology to  $\gamma$ -thionin from tobacco (Gu et al., 1992). In preliminary RNA gel blot analysis, the two mRNAs accumulated to high levels in the incompatible interaction. A full-length cDNA clone of pddThi was isolated from a cDNA library prepared from pepper fruits 24 and 48 h after inoculation with the fungus. The full-length clone was designated pPepThi (pepper thionin) and sequenced.

The pPepThi cDNA is 506 bp in length with 9 bp of 5'-untranslated region and 245 bp of 3'-untranslated region including the poly(A) tail (GenBank AF112443). The pPepThi clone represented a full-length cDNA of the 0.5 kb transcript identified by RNA gel blot analysis. The cDNA contained one open reading frame encoding a polypeptide of 9.5 kDa with 84 amino acids. The deduced amino acid sequence of

PepThi contained an N-terminal secretory signal peptide that was cleaved after glycine at position 25 (Figure 1). PepThi is a Cys-rich polypeptide containing the consensus Cys arrangement -C(...)C-X-X-X-C(...)G-X-C(...)C-X-C-.

A sequence alignment showed that the PepThi shared significant homology (identity and similarity: 50% and 64%, respectively) to a flower-specific  $\gamma$ -thionin from tobacco (Gu et al., 1992) and to several other  $\gamma$ -thionins from *Nicotiana* species and tomato (Milligan and Gasser, 1995; Figure 1). PepThi protein showed 29% identity for the whole coding region to a pepper defensin protein PepDef. PepThi did not have nucleotide sequence homology to thionins and was different from other  $\gamma$ -thionins. Thus, we assigned PepThi as a thionin-like protein.

### **Expression pattern and induction by fungal infection and wounding**

To examine the *PepThi* gene expression in various organs and its inducibility by fungal inoculation and wounding, RNA gel blot analysis was performed using total RNAs prepared from fruits, leaves, stems, and roots of pepper plants at 24 h after treatments. The expression of *PepThi* gene was observed in ripe fruits, leaves, stems, and roots (Figure 2). The basal and non-induced level of *PepThi* gene was higher in the leaves and roots than in the fruits and stems. In the fruits, the *PepThi* mRNA was highly induced by fungal infection and wounding. Also, the accumulation of the *PepThi* mRNA increased in the stems with fungal infection and wounding. However, the level of *PepThi* mRNA was not significantly changed in the leaves and roots by the treatments.

We hybridized the *PepDef* cDNA to the same blot that was used for the hybridization of *PepThi* cDNA. The basal level of *PepDef* gene was very high in the ripe fruit, and undetectably low in the unripe fruit (Figure 2). The *PepDef* mRNA was not detected in leaves, stems, and roots even after the treatments. *PepDef* protein is wound-inducible in the unripe fruit at 3 days after treatment (Meyer *et al.*, 1996). However, the accumulation of *PepDef* mRNA was not significantly induced in the unripe fruit by fungal infection and wounding for 24 h or 48 h. Interestingly, the level of *PepDef* mRNA was reduced in the ripe fruit by fungal infection and wounding. These phenomena were also observed in the ripe fruit by fungal infection and JA treatment (see Figures 3 and 4). These results suggest that *PepThi* and *PepDef* genes are developmentally and organ-specifically regulated, and the induction by fungal infection and wounding is also subject to developmental regulation.

#### **Differential induction by fungal infection during fruit ripening**

In our previous study for fungal morphogenesis on the surface of fruits, conidial germination, initial and mature infection hypha were observed at 2, 12, and 24 h after inoculations (HAIs), respectively (Oh *et al.* 1998). The initial anthracnose symptoms were detected only on the unripe fruit at 2 days after inoculation, resulting in typical sunken necrosis within 5 days after inoculation. To examine the time course of the induction of *PepThi* or *PepDef* mRNAs in response to the fungal infection, RNA gel blot analysis was performed with the ripe and unripe fruits at 0, 3, 6, 12, 24, 48, and 72 HAI using *PepThi* and *j1-1* cDNAs as probes. The uninoculated incompatible-ripe fruit

contained a basal level of *PepThi* mRNA (Figures 2 and 3). However, the expression of *PepThi* was rapidly induced in the ripe fruit upon fungal infection and reached a maximum at 48 and 72 HAI (Figure 3). In compatible-unripe fruits, the accumulation of *PepThi* mRNA was late, at 12 HAI, and reached its maximum level at 72 HAI.

Accumulation of *PepDef* mRNA in the unripe fruit was very low (Figure 3). As shown in Fig. 2, *PepDef* expression was suppressed by fungal infection in the ripe fruit. The transcript levels dropped until 48 HAI, and had begun to increase again 72 HAI. Since *PepDef* gene was highly expressed in the ripe fruit and *PepThi* gene was induced in the ripe fruit by the fungal infection, these genes may be involved in the defense mechanism during fruit ripening against the phytopathogen.

### **Induction and suppression during fruit ripening by JA and SA**

To identify the inducers of *PepThi* and *PepDef* gene expression from fruits, RNA gel blot analysis was performed with the unripe and ripe fruits treated with exogenous JA and SA for 24 h. The *PepThi* mRNA was highly accumulated in the unripe fruit compared to in the ripe fruit by SA at 5 mM (Figure 4). However, JA could not significantly induce the *PepThi* mRNA in both ripe and unripe fruits. The expression level of *PepDef* mRNA was not changed in both ripe and unripe fruits by SA. Interestingly, the expression of *PepDef* mRNA by JA increased in the unripe fruit, but decreased slightly in the ripe fruit. Taken together, these results suggest that the *PepThi* and *PepDef* genes are expressed via different signal transduction pathways during ripening.

## **Discussion**

Fungal-inducible thionin genes were identified in several plant/fungus interactions, such as in *Arabidopsis/Fusarium oxysporum* f.sp. *matthiolae* (Epple *et al.*, 1995), barley/*Stagonospora nodorum* (Titarenko *et al.*, 1993; Stevens *et al.*, 1996), and barley/the mildew fungus (Boyd *et al.*, 1994; Bohlmann *et al.*, 1998). Relevant to these findings, the accumulation of barley leaf thionin in papillae and in the cell wall surrounding the infection peg was higher in the incompatible interaction than that in the compatible one (Ebrahim-Nesbat *et al.*, 1989, 1993). Similar phenomena have been reported for many other plant and pathogen interactions. The induction of *PepThi* mRNA was observed to be faster in the incompatible interaction of ripe pepper fruits with the fungus (Figure 3).

The *PepThi* gene was induced during the early conidial germination of the fungus, before infection hyphae formation (Oh *et al.*, 1998) and even before appressorium formation (Kim *et al.*, 1999). These results suggest that signaling compounds released/produced during fungal germination result in the expression of *PepThi* gene in the epidermal cells of the incompatible-ripe fruit. Since the *PepThi* gene is expressed in various organs of pepper plants and its expression level is enhanced by fungal inoculation and wounding (Figure 2), *PepThi* thionin-like protein could play a role in conferring systemic protection for the plants against both biotic and abiotic stresses. Also, the induction of *PepThi* gene in the unripe fruit by SA (Figure 4) is consistent with a systemic protection role. SA plays an important role in the signal



transduction pathway leading to the systemic acquired resistance (Gaffney *et al.*, 1993).

The expression of the *PepDef* gene is regulated during fruit ripening. Similarly, several defensins and thionins are specifically expressed in reproductive organs, such as flowers in tobacco (Gu *et al.*, 1992) and *Arabidopsis* (Epple *et al.*, 1995), pistils in petunia (Karunanandaa *et al.*, 1994), and seeds in radish (Terras *et al.*, 1995). These findings suggest that both defensins and thionins are possibly involved in the defense mechanism for protecting the reproductive organ against pathogens or wounds. Further, thionins and other Cys-rich proteins exhibit synergistically enhanced antifungal activity (Terras *et al.*, 1993). Therefore, the concerted expression of both *PepDef* and *PepThi* genes during ripening could confer disease resistance in the ripe fruit during the early fungal infection process.

The responses to exogenous JA and SA treatments in pepper during fruit ripening are different for both *PepDef* and *PepThi* genes. JA as a chemical elicitor induces thionin genes in *Arabidopsis* (Epple *et al.*, 1995; Vignutelli *et al.*, 1998) and barley (Andresen *et al.*, 1992), and defensin genes in *Arabidopsis* (Penninckx *et al.*, 1996), in addition to other wound inducible genes (Hildmann *et al.*, 1992; Reinbothe *et al.*, 1994). SA also induces a thionin gene in barley leaf (Kogel *et al.*, 1995) as well as PR proteins (Ward *et al.*, 1991; Uknes *et al.*, 1992). A JA-independent wound induction pathway that shows opposite regulation to the JA-dependent one was identified in *Arabidopsis* (Rojo *et al.*, 1998). In the present study, the *PepThi* gene is strongly inducible in the unripe fruit by SA and wounding, but not by JA (Figure 4). These data indicate that the *PepThi* gene is expressed via a JA-independent wound signal

transduction pathway.

Since the *PepDef* gene is induced in the unripe fruit by JA, it is probably regulated via the octadecanoid pathway (Peña-Cortés *et al.*, 1995; Bergey *et al.*, 1996). The slightly suppression of the *PepDef* gene in the ripe fruit by JA and wounding is puzzling, since both JA in the unripe fruit result in the induction of *PepDef* mRNA. The possible explanation is that JA may elicit other signals that are able to activate genes in response to JA. These additional signals may result in the inhibition of *PepDef* expression in the ripe fruit.

This present study shows that a defensin and a thionin-like protein that may have defensive roles are deployed via different signal transduction pathways and may protect pepper fruits against the anthracnose fungus.

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